

SEQUENCE LISTING

<110> Lechler, Robert I.
Dorling, Anthony

<120> IMMUNOSUPPRESSION BY BLOCKING T CELL CO-STIMULATION SIGNAL 2 (B7/CD28
INTERACTION)

<130> 2292/0H795

<140> US 09/674,462

<141> 2001-05-08

<150> PCT/ GB99/01350

<151> 1999-04-30

<160> 27

<170> PatentIn Ver. 2.1

<210> 1

<211> 223

<212> PRT

<213> Sus scrofa

<400> 1

Met Ala Cys Ser Gly Phe Arg Ser His Gly Ala Trp Leu Glu Leu Thr
1 5 10 15

Ser Arg Thr Trp Pro Cys Thr Ala Leu Phe Ser Leu Leu Phe Ile Pro
20 25 30

Val Phe Ser Lys Gly Met His Val Ala Gln Pro Ala Val Val Leu Ala
35 40 45

Asn Ser Arg Gly Val Ala Ser Phe Val Cys Glu Tyr Gly Ser Ala Gly
50 55 60

Lys Ala Ala Glu Val Arg Val Thr Val Leu Arg Arg Ala Gly Ser Gln
65 70 75 80

Met Thr Glu Val Cys Ala Ala Thr Tyr Thr Val Glu Asp Glu Leu Thr
85 90 95

Phe Leu Asp Asp Ser Thr Cys Thr Gly Thr Ser Thr Glu Asn Lys Val
100 105 110

Asn Leu Thr Ile Gln Gly Leu Arg Ala Val Asp Thr Gly Leu Tyr Ile
115 120 125

Cys Lys Val Glu Leu Leu Tyr Pro Pro Pro Tyr Tyr Val Gly Met Gly
130 135 140

Asn Gly Thr Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser
145 150 155 160

Asp Phe Leu Leu Trp Ile Leu Ala Ala Val Ser Ser Gly Leu Phe Phe
165 170 175

Tyr Ser Phe Leu Ile Thr Ala Val Ser Leu Ser Lys Met Leu Lys Lys
180 185 190

Arg Ser Pro Leu Thr Thr Gly Val Tyr Val Lys Met Pro Pro Thr Glu
195 200 205

Pro Glu Cys Glu Lys Gln Phe Gln Pro Tyr Phe Ile Pro Ile Asn
210 215 220

<210> 2

<211> 672

<212> DNA

<213> Sus scrofa

<400> 2

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gccccaacctg cagtagtgct gccaacacgc cgggggtttg ccagcttgcgt gtgtgagttat 180
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atcacagctg tttctttgag caaaatgcta aagaaaagaa gtccttttac tacaggggtc 600
tatgtaaaaa tgcccccgac agagccagaa tgtgaaaagc aatttcagcc ttatttttatt 660
cccatcaatt ga 672

<210> 3

<211> 400

<212> PRT

<213> Artificial Sequence

<220>

<223> pCTLA4-Ig construct (Figure 4)

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Met Ala Cys Ser Gly Phe Arg Ser His Gly Ala Trp Leu Glu Leu Thr
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Ser Arg Thr Trp Pro Cys Thr Ala Leu Phe Ser Leu Leu Phe Ile Pro
20 25 30

Val Phe Ser Lys Gly Met His Val Ala Gln Pro Ala Val Val Leu Ala
35 40 45

Asn Ser Arg Gly Val Ala Ser Phe Val Cys Glu Tyr Gly Ser Ala Gly
50 55 60

Lys Ala Ala Glu Val Arg Val Thr Val Leu Arg Arg Ala Gly Ser Gln
65 70 75 80

Met Thr Glu Val Cys Ala Ala Thr Tyr Thr Val Glu Asp Glu Leu Thr
85 90 95

Phe Leu Asp Asp Ser Thr Cys Thr Gly Thr Ser Thr Glu Asn Lys Val
100 105 110

Asn Leu Thr Ile Gln Gly Leu Arg Ala Val Asp Thr Gly Leu Tyr Ile
115 120 125

Cys Lys Val Glu Leu Leu Tyr Pro Pro Pro Tyr Tyr Val Gly Met Gly
130 135 140

Asn Gly Thr Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser
145 150 155 160

Asp Gly Gly Ser Gly Gly Ala Ala Glu Pro Lys Ser Cys Asp Lys Thr
165 170 175

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser
180 185 190

Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
195 200 205

Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
210 215 220

Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
225 230 235 240

Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val
245 250 255

Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
260 265 270

Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr
275 280 285

Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu
290 295 300

Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys
305 310 315 320

Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
325 330 335

Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
340 345 350

Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
355 360 365

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
370 375 380

Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
385 390 395 400

<210> 4
<211> 722
<212> DNA
<213> Phage library

<400> 4

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acgcagactc cgtgaaggcc cggttccacca tctccagaga caattccaag aacacgctgt 240
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gtcgatatttt gtttgactat tgcccggaaat gtaccctggt caccgtctcg agtgggtggag 360
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cctcagcgtc tgggaccccc gggcagcggg tcaccatctc ttgttctggg agcagctcca 480
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tcatctatag gaataatcag cgccctcaag gggccctga ccgattctct ggctccaagt 600
ctggcacctc agcctccctg gccatcagtggc ggctccggc cgaggatgag gctgattatt 660
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<210> 5
<211> 240
<212> PRT
<213> Phage library

<400> 5

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Ala Ile Ser Gly Ser Gly Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Ala Gly Arg Ile Leu Phe Asp Tyr Trp Gly Gln Gly Thr Leu
100 105 110

Val Thr Val Ser Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly
115 120 125

Gly Ser Ala Leu Gln Ser Val Leu Thr Gln Pro Pro Ser Ala Ser Gly
130 135 140

Thr Pro Gly Gln Arg Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn
145 150 155 160

Ile Gly Ser Asn Tyr Val Tyr Trp Tyr Gln Gln Leu Pro Gly Thr Ala
165 170 175

Pro Lys Leu Leu Ile Tyr Arg Asn Asn Gln Arg Pro Ser Gly Val Pro
180 185 190

Asp Arg Phe Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile
195 200 205

Ser Gly Leu Arg Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Ala Trp
210 215 220

Asp Asp Ser Leu Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
225 230 235 240

<210> 6
<211> 729
<212> DNA
<213> Phage library

<400> 6
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ccaggctcca gggaaaggggc tggagtggtt ctcagctatt agtggtagtg gtggtagcac 180
atactacgca gactccgtga agggccgggt caccatctcc agagacaatt ccaagaacac 240
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caagtctggc acctcagcct ccctggccat cagtgggtc cggtccgagg atgaggctga 660
ttattactgt gcagcatggg atgacagcct ggtattcggc ggagggacca agctgaccgt 720
ccttaggtgc 729

<210> 7
<211> 738
<212> DNA
<213> Phage library

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ccggcagccc ccaggaaagg gactggagt gattgggtat atctattaca gtgggagcac 180
caactacaac ccctccctca agagtcgagt caccatatac gtacacacgt ccaagaacca 240
gttctccctg aagctgagct ctgtgaccgc tgccggacacg gccgtgtatt actgtgcaag 300
aatgcggaaag gataagttt actattgggg ccaaggtacc ctggtcaccg tctcgagtgg 360
tggaggcggt tcaggcggag gtggctctgg cggttagtgca cttcagtcgt tgctgactca 420
gccaccctca gcgtctggga cccccgggca gagggtcacc atctttgtt ctggaaagcag 480
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caagtctggc acctcagcct ccctggccat cagtgggtc cggtccgagg atgaggctga 660
ttattactgt gcagcatggg atgacagcct gttgtattc ggcggaggga ccaagctgac 720
cgtccttaggt gcggccgc 738

<210> 8
<211> 739
<212> DNA
<213> Phage library

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caggccctcg gacaaggct tgagtggatg ggaataatca accctagtgg tggttagcaca 180

caagctacgc acagaagttc cagggcagag tcaccatgac cagggacacg tccacgagca 240
cagtctacat ggagctgagc agcctgagat ctgaggacac ggccgtgtat tacttgcaa 300
gaatggctcc ctatgtaat acgctgttt tttggggcca aggtaccctg gtcaccgtct 360
cgagtggtgg aggcggttca ggcggaggtg gctctggcgg tagtgcactt cagtctgtgc 420
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ctgtacttgt catctatggt aaaaacaacc ggcctcagg gatcccagac cgattctctg 600
gctccagctc agggaaacaca gttccttga ccatcactgg ggctcaggcg gaagatgagg 660
ctgactatta ctgtaactcc cgggacagca gtggtttac tgtattcggc ggagggacca 720
agctgaccgt cctaggtc 739

<210> 9

<211> 729

<212> DNA

<213> Phage library

<400> 9

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gccagatgcc cgggaaaggc ctggagtggc tgggatcat ctatccttgt gactctgata 180
ccagatacag cccgtccttc caaggccagg tcaccatctc agccgacaag tccatcagca 240
ccgcctaccc gcagtggagc agcctgaagg cctcggacac ggccgtgtat tacttgcaa 300
gattttcgct tgggtggttt gactattggg gccaaggatc cctggtcacc gtctcgagt 360
gtggaggcgg ttcaggcgg a ggtggctctg gcgtagtgc acttgacatc cagttgaccc 420
agtctccatg ttccctgtctg catctgtagg agacagagtc accatcactt gccgggccc 480
tcagggcatt agcagttatt tagcctggta tcagcaaaaa ccagggaaag cccctaagct 540
cctggcttat gctgcattcca cttgcaaaag tgggtccca tcaaggatca gggcagtgg 600
atctggaca gaattcactc tcacaatcag cagcctgcag cctgaagatt ttgcaactta 660
ttactgtcaa cagcttaata gttaccgctt gacggtcggc caagggacca agctggaaat 720
caaacgtgc 729

<210> 10

<211> 240

<212> PRT

<213> Phage library

<400> 10

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
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Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Ala Ile Ser Gly Ser Gly Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65	70	75	80	
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys				
	85	90	95	
Ala Arg Ala Gly Arg Ile Leu Phe Asp Tyr Trp Gly Gln Gly Thr Leu				
	100	105	110	
Val Thr Val Ser Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly				
	115	120	125	
Gly Ser Ala Leu Gln Ser Val Leu Thr Gln Pro Pro Ser Ala Ser Gly				
	130	135	140	
Thr Pro Gly Gln Arg Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn				
	145	150	155	160
Ile Gly Ser Asn Tyr Val Tyr Trp Tyr Gln Gln Leu Pro Gly Thr Ala				
	165	170	175	
Pro Lys Leu Leu Ile Tyr Arg Asn Asn Gln Arg Pro Ser Gly Val Pro				
	180	185	190	
Asp Arg Phe Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile				
	195	200	205	
Ser Gly Leu Arg Ser Glu Asp Glu Ala Ser Tyr Tyr Cys Ala Ala Trp				
	210	215	220	
Asp Asp Ser Leu Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly				
	225	230	235	240

<210> 11
<211> 246
<212> PRT
<213> Phage library

<400> 11
Met Ala Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro
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Ser Glu Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Val Ser
20 25 30

Ser Gly Ser Tyr Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly
35 40 45

Leu Glu Trp Ile Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Asn Tyr Asn
50 55 60

Pro Ser Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn
65 70 75 80

Gln Phe Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val
85 90 95

Tyr Tyr Cys Ala Arg Met Arg Lys Asp Lys Phe Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
115 120 125

Gly Ser Gly Gly Ser Ala Leu Gln Ser Val Leu Thr Gln Pro Pro Ser
130 135 140

Ala Ser Gly Thr Pro Gly Gln Arg Val Thr Ile Ser Cys Ser Gly Ser
145 150 155 160

Ser Ser Asn Ile Gly Ser Asn Tyr Val Tyr Trp Tyr Gln Gln Leu Pro
165 170 175

Gly Thr Ala Pro Lys Leu Leu Ile Tyr Arg Asn Asn Gln Arg Pro Ser
180 185 190

Gly Val Pro Asp Arg Phe Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser
195 200 205

Leu Ala Ile Ser Gly Leu Arg Ser Glu Asp Glu Ala Asp Tyr Tyr Val
210 215 220

Ala Ala Trp Asp Asp Ser Leu Phe Val Phe Gly Gly Gly Thr Lys Leu
225 230 235 240

Thr Val Leu Gly Ala Ala
245

<210> 12
<211> 242
<212> PRT
<213> Phage library

<400> 12
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Arg Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Ile Ile Asn Pro Ser Gly Gly Ser Thr Ser Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Val Ala Pro Tyr Val Asn Thr Leu Val Phe Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser Gly Gly Gly Ser Gly Gly Gly Gly
115 120 125

Ser Gly Gly Ser Ala Leu Ser Ser Glu Leu Thr Gln Asp Pro Ala Val
130 135 140

Ser Val Ala Leu Gly Gln Thr Val Arg Ile Thr Cys Gln Gly Asp Ser
145 150 155 160

Leu Arg Ser Tyr Tyr Ala Ser Trp Tyr Gln Gln Lys Pro Gly Gln Ala
165 170 175

Pro Val Leu Val Ile Tyr Gly Lys Asn Asn Arg Pro Ser Gly Ile Pro
180 185 190

Asp Arg Phe Ser Gly Ser Ser Gly Asn Thr Ala Ser Leu Thr Ile
195 200 205

Thr Gly Ala Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Asn Ser Arg
210 215 220

Asp Ser Ser Gly Phe Thr Val Phe Gly Gly Thr Lys Leu Thr Val
225 230 235 240

Leu Gly

<210> 13
<211> 240
<212> PRT
<213> Phage library

<400> 13

Gln Val Gln Leu Leu Gln Ser Ala Ala Glu Val Lys Lys Pro Gly Glu
1 5 10 15

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Thr Ser Tyr
20 25 30

Trp Ile Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met
35 40 45

Gly Ile Ile Tyr Pro Gly Asp Ser Asp Thr Arg Tyr Ser Pro Ser Phe
50 55 60

Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr
65 70 75 80

Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Phe Ser Leu Gly Gly Phe Asp Tyr Trp Gly Gln Gly Thr Leu
100 105 110

Val Thr Val Ser Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly
115 120 125

Gly Ser Ala Leu Asp Ile Gln Leu Thr Gln Ser Pro Ser Phe Leu Ser
130 135 140

Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly
145 150 155 160

Ile Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro
165 170 175

Lys Leu Leu Val Tyr Ala Ala Ser Thr Leu Gln Ser Gly Val Pro Ser
180 185 190

Arg Phe Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser
195 200 205

Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Leu Asn
210 215 220

Ser Tyr Arg Leu Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg
225 230 235 240

<210> 14
<211> 742
<212> DNA
<213> Homo sapiens

<400> 14
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cctggccctg cactctcctg tttttcttc tcttcatccc tgtcttctgc aaagcaatgc 180
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agtatgcac tccaggcaaa gccactgagg tccgggtgac agtgcctcg caggctgaca 300
gccaggtgac tgaagtctgt gcggcaacct acatgatggg gaatgagttg accttcctag 360
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tgagggccat ggacacggga ctctacatct gcaaggtgga gctcatgtac ccaccgccat 480
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ttctcctcac agctgtttt ttgagcaaaa tgctaaagaa aagaagccct cttacaacag 660
gggtctatgt gaaaatgccc ccaacagagc cagaatgtga aaagcaattt cagccttatt 720
ttattccat caattgagaa tt 742

<210> 15
<211> 223
<212> PRT
<213> Homo sapiens

<400> 15
Met Ala Cys Leu Gly Phe Gln Arg His Lys Ala Gln Leu Asn Leu Ala
1 5 10 15
Thr Arg Thr Trp Pro Cys Thr Leu Leu Phe Phe Leu Leu Phe Ile Pro
20 25 30
Val Phe Cys Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala
35 40 45
Ser Ser Arg Gly Ile Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Gly
50 55 60
Lys Ala Thr Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln
65 70 75 80
Val Thr Glu Val Cys Ala Ala Thr Tyr Met Met Gly Asn Glu Leu Thr
85 90 95
Phe Leu Asp Asp Ser Ile Cys Thr Gly Thr Ser Ser Gly Asn Gln Val
100 105 110
Asn Leu Thr Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile
115 120 125

Cys Lys Val Glu Leu Met Tyr Pro Pro Pro Tyr Tyr Leu Gly Ile Gly
130 135 140

Asn Gly Thr Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser
145 150 155 160

Asp Phe Leu Leu Trp Ile Leu Ala Ala Val Ser Ser Gly Leu Phe Phe
165 170 175

Tyr Ser Phe Leu Leu Thr Ala Val Ser Leu Ser Lys Met Leu Lys Lys
180 185 190

Arg Ser Pro Leu Thr Thr Gly Val Tyr Val Lys Met Pro Pro Thr Glu
195 200 205

Pro Glu Cys Glu Lys Gln Phe Gln Pro Tyr Phe Ile Pro Ile Asn
210 215 220

<210> 16
<211> 773
<212> DNA
<213> Homo sapiens

<400> 16
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ctcctgccgc tggccttgct gctccacgcc gccaggccga gccagttccg ggtgtcgccg 120
ctggatcgga cctggAACCT gggcgagaca gtggagctga agtgcgcagg tctgtgtcc 180
aaccgcacgt cgggctgctc gtggctcttc cagccgcgcg gcgcgcgcgc cagtcccacc 240
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ttctcgggca agagggttggg ggacacccctc gtccctaccc tgagcgactt ccgcgcagag 360
aacgaggggct actatttctg ctcggccctg agcaactcca tcatgtactt cagccacttc 420
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gcgcacca tcgcgtcgca gccctgtcc ctgcgcggcagg aggcgtgccc gccagcggcg 540
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aggaacccaa gacgtgtttg caaatgtccc cggcctgtgg tcaaatacgag agacaagccc 720
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<210> 17
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 17
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<210> 18
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 18
taatgaattc tcaattgatg ggaataaaat aag 33

<210> 19
<211> 60
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 19
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<210> 20
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 20
gagctgaaac gggcgccgc agaac 25

<210> 21
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 21
ctggcctgca gcattcagat cc 22

<210> 22
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 22
ttcaaagctt caggatcctg aaaggaaaa 30

<210> 23
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 23
taatgaattc tcaattgatg ggaataaaat aag 33

<210> 24
<211> 76
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 24
gatgtagata tcacaggcga agtcgacacc accggagcca ccaattacat aaatctggc 60
tccgttgcct atgcc 76

<210> 25
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 25
tcgcgcctaa gcttcgagcc aagcagcgt 29

<210> 26
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 26

taatgaattc tcaattgatg ggaataaaat aag

33

<210> 27

<211> 73

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 27

cataggcaac ggagcccaga tttatgtaat tggtggctcc ggtgggtgtcg acttcgcctg 60

tgatatctac atc 73